

## STIC Database Tracking Number 135947

TO: Ruixiang Li

Location: rem/4d75/4c70

Art Unit: 1646

Tuesday, November 02, 2004

Case Serial Number: 10/763854

101 021.775

From: Edward Hart

**Location: Biotech-Chem Library** 

**REM-1A55** 

Phone: 571-272-2512

edward.hart@uspto.gov

## Search Notes

Examiner Li,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

**Edward Hart** 



encoding nucleic acids. The GPCR protein and nucleic acids of the invention are useful in the treatment of a disease or condition mediated by a human protease. The GPCR protein of the invention is useful for: the development/identification of therapeutic proteins; assays designed to quantitatively determine levels of the protein in biological fluids; interaction of the GPCR and a molecule with which it normally interacts; and treating a disorder characterised by an absence of, or inappropriate expression of the GPCR protein. The GPCR nucleic acids of the invention are useful in diagnostic assays to identify changes in the GPCR nucleic acid that lead to pathology; controlling GPCR expression, and in gene therapy to treat patients with aberrant GPCR gene expression. The GPCR nucleic acids can also be used in the production of transgenic animals

180

180 240 120

9 9

Gaps

ö

Length 337; Indels 1 MNEPLDYLANASDFPDYAAAFGNCTDENIPLKOHYLPVIYGIIFLVGFPGNAVVISTYIF

유 ò 셤 ö 엄 ò 셤 à 셤 ઠે 셤

61 KMRPWKSSTIIMLNLACTDLLYLTSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSS 61 KARPWKSSTIIMLNLACTDLLYLTSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSS 121 ILFLICESIFRYCVIIHPMSCFSIHKTRCAVVACAVVWIISLVAVIPMTFLITSTNRTNR

1 MNEPLDYLANASDFPDYAAAFGNCTDENIPLKMHYLPVIYGIIFLVGFPGNAVVISTYIF

100.0%; Score 1771; DB 5; 100.0%; Pred. No. 1.1e-194; ive 0; Mismatches 0;

Best Local Similarity 100 Matches 337; Conservative

Query Match

Sequence 337 AA;

240

180

121 ILFLICPSIFRYCVIIHPMSCFSIHKTRCAVVACAVVWIISLVAVIPWTFLITSTNRTNR

181 SACEDITSSBELNTIKWYNLILTATTFCLPLVIVTLCYTTIHTLTHGLQTDSCLKQKAR

SACLDLISSDELNTIKMYNLILTATTFCLPLVIVTLCYTTIIHTLTHGLQTDSCLKQKAR

181

301 LYVVVSDNFQQAVCSTVRCKVSGNLEQAKKISYSNNP 337 LYVVVSDNFQQAVCSTVRCKVSGNLEQAKKISYSNNP 337

301

AAU77600 standard; protein; 337 AA

AAU77600

RESULT

AAU77600;

RLTILLLLARYVCFLPFHILRVIRIESRLLSISCSIBNQIHEAYIVSRPLAALNTFGNLL

241

240 240

```
241 RITILLLLAFYVCFLPFHIDRVIRIESRLLSISCSIENQIHEAYIVSRPLAALNTFGNLL 300
KWRPWKSSTIIMINLACTDLLYLTSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSS
                                                                                              121 ILFLTCPGIFRYCVIIHPMSCFSIHKTRCAVVACAVVWIISLVAVIPMTFLITSTNRTNR
                                                                                                                                              61 KARPWKSSTIIMLNLACTDLLYLTSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSS
                                                                                  LICESIFRYCVIIHPMSCFSIHKTRCAVVACAVVWIISLVAVIPMTFLITSTNRTNR
                                                                                                                               181 SACLDLISSDEKNTIKWYNLILIATTFCLPLVIVTLCYTTIIHTLTHGLQTDSCLKQKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated G-protein coupled receptor peptide useful for treating disorder characterized by absence of, in appropriate or unwanted expression of the receptor protein, and as immunogens to raise
                                                                                                                                                                                                                                                                                                                                                                                                     Human, chromosome 13; purinergic GPCR; G-protein coupled receptor;
signal transduction; human protease, GPCR disorder; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                               Human purinergic-related G-protein coupled receptor (GPCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beasley
                                                                                                                                                                                                                                           LYVVVSDNFQQAVCSTVRCKVSGNLEQAKKISYSWNP 337
                                                                                                                                                                                                                            KISYSNNP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Di Francesco V,
                                                                                                                                                                                                                          LYVVVSDNFQQAVCSTVRCKVSGNLEQAR
                                                                                                                                                                                                                                                                                                         AA014027 standard; protein; 337 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cravchik A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-2001; 2001WO-US015957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAY-2000; 2000US-0205196P.
08-AUG-2000; 2000US-00634656.
                                                                                                                                                                                                                                                                                                                                                                                                                                transgenic animal; receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAK98323, AAK98324.
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (APPL-) APPLERA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-075312/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhao Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200187980-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                         30-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibodies
                                                                                  121
                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                 AA014027;
                                                                                                                                                                                                                                                301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wei M,
                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                               AA01402
                                                        셤
                                                                               ò
                                                                                                       g
                                                                                                                                                   g
                                                                                                                             ò
                                                                                                                                                                           ò
                                                                                                                                                                                                 d
                                                                                                                                                                                                                           ð
```

Human; P2Y1-like G protein-coupled; receptor; GPCR; infection; pain; cancer; anorexia; bulnia; asthma; hypotension; central nervous system disease; acute heart failure; hypertension; urinary retention; osteoporosis; diabetes; angina pectoris; myocardial infarction; ulcer; inflammation; alleryy; multiple sclerosis; benign prostatic hypertrophy; psychosis; neurological disorder; dyskinesia; HIV; human immunodeficiency virus infection; CNS disorder; deaktinesia; HIV; human immunodeficiency virus infection; CNS disorder; dementia; severe mental retardation; Huntington's disease; Tourette's syndrome. Human P2Y1-like G protein-coupled receptor. (first entry) WO200214511-A2 05-JUN-2002 21-FEB-2002. 

10-AUG-2001; 2001WO-EP009243

The present specifically claimed sequence represents a human purinergic-related G-protein coupled receptor (GPCR) encoded by a gene on chromosome 13. GPCRs constitute a major class of proteins responsible for signal transduction within a cell. Upon binding of a ligand to the extracellular portion of a GPCR, a signal is transduced resulting in a biological or physiological change within the cell. The GPCR proteins can be divided inco five families, family I contains the purinergic GPCRs (e.g. the P2Y receptors are characterised by their selective responsiveness towards ATP and its analogues, some also respond to UTP. The invention comprises a human G-protein coupled receptor protein and

Claim 1; Fig 2; 64pp; English

(G-protein coupled receptor) protein.

Human AXOR89

can pe

(first entry)

16-JUL-2002

AAE21803;

```
The invention relates to a purified human P2Y1-like G protein-coupled receptor (GPCR) polypeptide and the nucleic acids encoding it (including 5' and 3 sequences, promoters, fragments, variants, or a sequence encoding a protein at least 50% identical to the GPCR). Also included are an expression vector and the identification of modulators of the GPCR especially those that reduce the activity of the GPCR. The nucleic acid is useful for detecting a polynucleotide encoding the GPCR, in a biological sample. The GPCR and nucleic acid are useful for screening for agents which carease the activity of the GPCR and for modulators of the GPCR. The modulator or agent useful for modulating the activity of P2Y1-like G modulator or agent useful for modulating the activity of P2Y1-like G protein-coupled receptor in a disease such as bacterial, fungal, protozoan, and viral infection, pain, cancer, anorexia, bulimia, asthma, central nervous system (CNS) disease, acute heart failure, hypotension, hypertension, unlear, inflammation, allergy, multiple sclerosis, benign prostatic hypertrophy, psychotic and neurological disorders, construction, protein immantion, and neurological disorders, diskinesias, HIV virus infection (human immunodeficiency virus), CNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders such as Parkinson's disease, anxiety, schizophrenia, manic
depression, delirium, dementia, severe mental retardation, Huntington's
disease and Tourette's syndrome. The present sequence represents the P2Y1
                                                                                                                                                                                                                                                       Novel human P2X1-like G protein-coupled receptor polypeptide which eregulated for treating infection, pain, cancer, diabetes, anorexia, asthma, hypertension, neurological disorder and dyskinesia.
                                                                                                                                                                                                                                                                                                                                                             Claim 25; Fig 2; 118pp; English
                           14-AUG-2000; 2000US-0224989P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 like GPCR of the invention
                                                                                                                                                                             WPI; 2002-257607/30.
N-PSDB; ABK11381.
                                                                       (FARB ) BAYER AG
```

Sequence 337 AA;

```
ö
                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                          181 SACLDLTSSDELNTIKWYNLILTATTFCLPLVIVTLCYTTIIHTLTHGLQTDSCLKQKAR 240
                                                                                                                                           KWRPWKSSTIIMLNLACTDLLYLTSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSS 120
                                                                                                                                                                                                             ILFLICESIFRYCVIIHPMSCFSIHKTRCAVVACAVVWIISLVAVIPWTFLITSTNRTNR 180
                                                                                                                                                                                                                                                 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVVACAVVWIISLVAVIPMTFLITSTNRTNR 180
                                                                                                                                                                                                                                                                                                                                                           RLTILLLLAFYVCFLPFHILRVIRIESRLLSISCSIENQIHEAYIVSRPLAALNTFGNLL 300
                                                                                                                                                                                                                                                                                                                                                                                1 MNEPLDYLANASDFPDYAAAFGNCTDENIPLKMHYLPVIYGIIFLVGFFGNAVVISTYIF 60
                                                                                                       1 MNEPLDYLANASDFPDYAAAFGNCTDENIPLKMHYLPVIYGIIFLVGFPGNAVVISTYIF 60
                                                                                                                                                                SACLDLTSSDELNTIKWYNLILTATTFCLPLVIVTLCYTTIHTLTHGLQTDSCLKQKAR
                                   Gaps
                                   .
.
100.0%; Score 1771; DB 5; Length 337; 100.0%; Pred. No. 1.1e-194;
                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYVVVSDNFQQAVCSTVRCKVSGNLEQAKKISYSNNP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                 301 LYVVVSDNFQQAVCSTVRCKVSGNLEQAKKISYSNNP 337
                                   Mismatches
                                     0.
                  Best Local Similarity 100.
Matches 337; Conservative
                                                                                                                                           61
                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                             241
 Query Match
                                                                                                       g
                                                                                                                                                                                                                                               요
                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                 ठे
                                                                                                                                           ò
                                                                                                                                                                           셤
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                         ò
```

AE21803 ID AAE21803 standard; protein; 337

ö

```
The invention relates to an isolated AXOR89 polypeptide (G-protein coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide and polynucleotide encoding the polypeptide, is useful for identifying agonists and antagonists (or inhibitors) that are potentially useful in treating conditions associated with an AXOR89 imbalance, such as barterial, fungal or protezoan infections, cancers, pain, asthma, barterial, purpose of protezoan infections, cancers, bulinia, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, cangina pectoris, mycocardial infarction, shroke, ulcers, allergies, benign procestic, mycocardial infarction, shroke, ulcers, allergies, benign proteins, mycocardial infarction, shroke, ulcers, allergies, benign proteins, and shunington's bisease or files dela Tourette's dyskinesias, such as Huntington's Disease or files dela Tourette's syndrome. The polynucleotide sequence may also be used for chromosome localisation or tissue expression studies. The AXOR89 is used as a various contraction or to produce fusion proteins. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FNLYSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IR 180
                                           Human, AXOR89 polypeptide, G-protein coupled receptor; vaccine; receptor; infection; cancer; pain; asthma; Parkinson's Disease; diabetes; obesity; shorexia; bulima; acute heart failure; hypotemaion; hyperension; ulcer; skoke; urinary retention; osteoporosis; angina pectoris; schizophrenia; myocardial infarction; allergy; benign prostatic hypertrophy; migraine; comptting; psychotic; neurological disorder; anxiety; manic depression; dementia; dyskinesia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel AXOR89 polypeptide and polynucleotide encoding it, useful for identifying agonists and antagonists in the treatment of diseases associated with an AXOR89 impalance, such as cancers, diabetes or asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNAVVISTYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WISTYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILFLICESIERXCVIIHPMSCFSIHKTRCAVVACAVWIISLVAVIEMTFLITSTNRTNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KMRPWKSSTIIMLNLACTDLYLTSLPFLIHYYASGENWIFGDFWCKFIRFSFHFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 KMRPWKSSTIIMLNLACTDLLYLTSLPFLIHYYASGENWIFGDFMCKFIRFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNEPLDYLANASDFPDYAAAFGNCTDENIPLKMHYLPVIYGIIFLVGFPGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNEPLDYLANASDFPDYAAAFGNCTDENIPLKMHYLPVIYGIIFLVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1771; DB 5; 100.0%; Pred. No. 1.1e-194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 30; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-2000; 200pus-00569137.
                                                                                                                                                                                                                                                                                                                                                    W01GB-00011437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Elshourbagy N, Shabon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-332558/37. N-PSDB; AAD34278.
                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINB
(SMIK ) SMITHKLINB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 337 AA;
                                                                                                                                                                                                                                    Homo saptens.
                                                                                                                                                                                                                                                                                                                                                    10-MAY-2001;
                                                                                                                                                                                                                                                                                                            13-FEB-2002
                                                                                                                                                                                                                                                                       GB2365012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

us-10-763-854-1.rng

```
The invention relates to an isolated P2Y-like receptor polypeptide

(ABB33818-ABB83819) which is also referred to in the specification as

altered to the specification as a stranged by the specification as a tragonist, which modulates P2Y receptor activity is useful to treat a substance with a disorder that is responsive to P2Y-like receptor modulation. The disorder is a disease of immunity or inflammation. The cubstance way also be used to manufacture a medicine for the treatment or prophylaxia of a disorder that is responsive to stimulation or modulation of P2Y-like receptor activity. Disorders which may be treated include colon cancers aschma, COPD, Crohn's disease, irritable bowel syndrome, of partners and colitis, inflammatory bowel syndrome, ulcerative colitis, rheumatoid arthritis, viral diseases, bacterial infections, autoimmune diseases, dermaitis, glomerulonephritis allergies, allergic colitis, inflammatory pain and general inflammation such as tendonitis, polymyositis or prostatitis. The invention provides alternative confine present sequence is that the P2Y-like receptor variant encoding gene of the passent sequence is that the P2Y-like receptor variant encoding gene
An isolated P2Y-like receptor polypeptide (HIPHUM 0000037) which can be used for the identification of agonists and antagonists which may be used to treat an immune or inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 C; 189 G; 304 T; 0 U; 0 Other;
                                                                                                                    aim 5; Page 28-29; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1014 BP; 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence
of the invention
```

ö 480 540 540 120 240 240 360 360 420 480 ATTITGACIGCAACTACTITCIGCCICCCTIGGIGAIAGIGACACTITGCIAIACCAÒG. 660 120 180 180 CTATGCCAGTGGCGAAAACTGGATC 300 300 420 ACCTA 600 TCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAAACTG 600 9 9 GCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTCC AAAATGAGAACCTTGGAAGAGCAGCACCATCATAATGCTGAACCTGGCCTGCACAGATCTG CATTCACCCAATGAGC GACCAACAGA TAGCAAATGCTTCTGATTTCCCCGATTATGCAGCTGCT TTATGCTGAACCTGGCCTGCACAGATCTG Trickacarricarcraacrirarccccricaccrickarricaacricararacacc CCAACAGA ITTAGCAAATGCTTCTGATTTCCCCCGATTATGCAGCTGCT CATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT ATGCCAGTGGCGAAAACTGGATC CATTTCAACCTGTATAGCAGC SGCAATGCAGTAGTGATATCCACTTACATTTTC ATCATTCACCCAATGAGC GGTGTGGATCATT cocactoaagargcacraccroccrotrarrrar TGTGGATCATT Gaps Score 1012.4; DB 6; Length 1014; Pred. No. 5.8e-289; ); Mismatches 1; Indels 0; TCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTA rcacregradericrearreceargacerrerrearcacarcaaccage TCACTGGTAGCTGTCATTCCGATGACCTTCTTGATCACATCAACAACA TGCTTTTCCATTCACAAACTCGATGTGCAGTTGTAGCCTGTGCTGT TGCTTTTCCATTCACAAACTCGATGTGCAGTTGTAGCCTGTGC Arcercirceicacerericacearerrececiaerer ATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGT TGGAGATTTCATGTGTAAGTTTATCCGCTTCAGC 241 crerarcidaccacciccicirccidaricaciad CIGIAICIGACCAGCCICCCCTICCIGATICAC AAAATGAGACCTTGGAAGAGCAGCACCATCA GGCATTATCTTCCTCGTGGGATTTCC TTTGGAAATTGCACTGATGAAAACA 0; TTTGGAAATTGCACTGATGAAAA Argaargagccacragacrar 1 ATGAATGAGCCACTAGACT 99.66 Query Match
Best Local Similarity 99.9
Matches 1013; Conservative ч 181 361 481 61 61 121 121 181 241 301 301 361 421 421 481 601

g

ö 유  $\delta$ d े d

g

ò 엄

8 g ò ò

පු ò ద  $\delta$ 엄 8

780 840 840 960 960 9 720 720 780 900 900 Human purinergic-related G-protein coupled receptor (GPCR) cDNA sequence. 601 ATTITGACTGCAACTATTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACG TAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTG caecaegererecreaacaereaearecaaa ATTATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAAGCACGA **QATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATC** 841 CATGAAGCTTACATCGTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTA Novel isolated G-protein coupled receptor peptide useful for treating disorder characterized by absence of, in appropriate or unwanted expression of the receptor protein, and as immunogens to raise GATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATC CTATATGTGTGGTCAGCGACATTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA AGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCCATATCTTG ATTAGTTACTCAAACAACCCTTGA 1014 Human, chromosome 13, purinergic GPCR, G-protein coupled receptor, signal transduction, human protease; GPCR disorder, gene therapy; 照; Beasley "G-protein coupled receptor" Francesco V, GTAAGCGGGAACCTTGAGCAAGCAAGAA Location/Qualifiers
1. .1014
/\*tag= a
/product= "G-protein craraferefreercaeceacaetae 검 ВР AAK98323 standard; cDNA; 1014 17-MAY-2001; 2001WO-US015957. 18-MAY-2000; 2000US-0205196P. 08-AUG-2000; 2000US-00634656. Cravchik A, transgenic animal; gene; ss. (first entry) (APPL-) APPLERA CORP WFI; 2002-075312/10. P-PSDB; AA014027. 781 AGGGTCATT CATGAAGCT Zhao Q, WO200187980-A2. 781 AGGG Homo sapiens. 30-APR-2002 22-NOV-2001 antibodies 661 AAK98323; 661 841 901 901 961 961 Wei M, Key AAK98323 RESULT ծ 셤 ઠ g ઠ 셤 ò g  $\dot{\delta}$ g ò 硆 

Claim 23; Fig 1; 64pp; English

ò

6 The present specifically claimed human cDNA sequence (located 780

780

661

721 721 721 781

8 8

781 AGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATC

841

841

8 6 8 6

CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACACCTTTGGTAACCTGTTA

840

900

```
chromosome 13) encodes a purinergic-related G-protein coupled receptor (GPCR) of the invention. GPCRs constitute a major class of proteins responsible for signal transduction within a cell. Upon binding of a ligand to the extracellular portion of a GPCR, a signal is transduced resulting in a biological or physiological change within the cell. The GPCR proteins can be divided into five families, family I contains the curacterised by their selective responsiveness towards ATP and its characterised by their selective responsiveness towards ATP and its characterised by their selective responsiveness towards ATP and its contains the characterised by their selective responsiveness towards ATP and its contains the controlled receptor protein and encoding nucleic acids. The GPCR protein and nucleic acids of the invention are useful in the treatment of the invention is useful for: the development/identification of the invention is useful for: the development/identification of the activity of the GPCR, or the interacting a disorder characterised by an absence of, or imappropriate expression of the GPCR and a molecule with which it normally interacts; and treating a disorder characterised by an absence of, or imappropriate expression of the GPCR and a molecule GPCR nucleic acids of the invention are useful in diagnostic assays to identify changes in the GPCR nucleic acid that lead to pathology; controlling GPCR gene expression. The GPCR nucleic acids can also be used in the production of transgenic animals
```

Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other; v. Match 99 A; Score 1012.4: DB 6: Length 101.

ö 360 360 TITGGAAATIGCACTGAIGAAAACAICCCACTCAAGAIGCACTACCICCTGTTAITAT 120 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTGATAGTGATATCCACTTACATTTTC 180 240 240 CTGTATCTGACCAGCCTCCCCTTCCTGATTCACTATGCCAGTGGCGAAAACTGGATC 300 300 420 Arcererrecreacererrreacearerreceeracirerererexeerexeeee 480 480 9 AAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCTGCACAGATCTG CTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGTGTGGGGGAAAACTGGATC TITGGAGATITCAIGIGIAAGITTAICCGCTICCAGCTICCAITICAACCIGTAIAGCAGC recririrecarreaaacreaarerecagricaaecrerecererecarrearr 1 ATGAATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCGGATTATGCAGCTGCT ATGAATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCGGATTATGCAGCTGCT rrrdgaaarrdcacrdardaaaacarcccacrcaagardcacraccrccrgrrarrrar GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTC AAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTG TITIGGAGATITICATGIGTAAGITTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC ATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGC TGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGGATCATT Gaps DB 6; Length 1014; ô 1; Indels Score 1012.4; DB 6 Pred. No. 5.8e-289; 0; Mismatches 1; Query Match 99,04; Best Local Similarity 94,94; Matches 1013; Conservative 61 181 241 301 361 181 121 241 301 361 421 421 셤 ò q à d 8 g ò В 8 쉼  $\stackrel{>}{\circ}$ 셤 ò q ð

ATTTTGACTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACG 660

601

ATTITGACTGCAACTACTITCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACG

TCACTGGTAGCTGTCATTCCGATGACCTTCTTGATCACAACAACAGGACCAACAGA 540

481 481 541

8 6 6 6

рe 960 Human; ds; gene; P2Y1-like G protein-coupled receptor; GPCR; infection; pain; cancer; anorexia; bulimia, asthma; hypotension; central nervous system disease; acute heart failure; hypertension; urinary retention; osteoporosis; diabetes; angina pectoris; myocardial infarction; ulcer; inflammation; allergy; multiple sclerosis; benign prostatic hypertrophy; psychosis; neurological disorder; dyskinesia; HIV; human immunodeficiency virus infection; CNS disorder; Parkinson's disease; anxiety; schizophrenia; manic depression; delirium; Tourette's syndrome. Novel human P2Y1-like G protein-coupled receptor polypeptide which can regulated for treating infection, pain, cancer, diabetes, anorexia, asthma, hypertension, neurological disorder and dyskinesia. CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA 1014 GIAAGCGGGAACCTIGAGCAAGCAAAAATTAGTTACTCAAACAACCTTGA Human DNA encoding P2Y1-like G protein-coupled receptor. /product= "P2Y1-like GPCR" Location/Qualifiers 1. .1014 /\*tag= a ВР 14-AUG-2000; 2000US-0224989P. ABK11381 standard; DNA; 1014 10-AUG-2001; 2001WO-EP009243 (first entry) WPI; 2002-257607/30. P-PSDB; AAU77600. (FARB ) BAYER AG Ramakrishnan S; WO200214511-A2 Homo sapiens 05-JUN-2002 21-FEB-2002 ABK11381; 901 901 196 961 RESULT 9 ò à

The invention relates to a purified human P2XI-like G protein-coupled receptor (GPCR) polypeptide and the nucleic acids encoding it (including receptor (GPCR) polypeptide and the nucleic acids encoding it (including 5 ' and 3 sequences. promoters, fragments, variants, or a sequence can expension vector comprising the function to the GPCR and so included are an expression vector comprising the mucleic acid, a host cell containing those that reduce the activity of the GPCR. The nucleic acid is useful for detecting a polymucleotide encoding the GPCR in a biological sample. The GPCR and nucleic acid are useful for screening for agents which decrease the activity of the GPCR and for modulators of the GPCR. The modulator or agent useful for modulators of the GPCR. The modulator or agent useful for modulating the activity of P2XI-like G protein-coupled receptor in a disease such as bacterial, fundal, asthma, central nervous system (CNS) disease, acute heart failure, hypotension, hypotension, uninary retention, osteoporosis, diabetes, analysin percention, ulcer, inflammation, allergy, multiple sclerosis, discretes such as Parkinson's disease, anxiety, schizophrenia, manic disorders such as Parkinson's disease, anxiety, schizophrenia, manic disorders the present sequence encodes the P2XI-Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other; [0.0] Claim 1; Fig 5; 118pp; English. like GPCR of the invention 61 61 121 g ò Db à g à

ö 240 300 300 360 360 420 420 480 480 540 540 TCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTA 600 ATTITGACIGCAACTACTITCIGCCICCCCTIGGIGAIAGIGACACTITGCIAIACCACG 660 180 240 120 120 180 9 9 rcacregradereretreceareacerretreareacereaecaacageaceaeaa GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGGAGATATCCACTTACATTTTC AAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTG CTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACTGGATC crerarcreaccaecerecerrecrearreacracrareceaeresceaere TITGGAGATITCATGTGTAAGTITATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC rrrocadarrrcardranderrrandoderrcadricarrrocarrrocandered ATCCTCTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGATCATCACCCAATGAGC TGCTTTTCCATTCACAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCATT TGCTTTTCCATTCACAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGATCATT 1 AIGAAIGAGCCACTAGAACTATTTAGCAAATGCTTCTGATTTCCCCGGATTATGCAGCTGCT Archarcacccacrarrragcaharccrrcrcarrrcccccarrarcacccc Gaps Query Match

99.8%; Score 1012.4; DB 6; Length 1014;
Best Local Similarity 99.9%; Pred. No. 5.8e-289;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; 181 181 241 241 301 301 361 361 421 421 481 481 541 541 601

g

 $\dot{\delta}$ 

Db

 $\stackrel{>}{\circ}$ 엄 à g δ Ob δ g

 $\delta$ 

Db

ઠે

à

The invention relates to a method for screening G protein-coupled receptor (GPCR) genes (ABZ42870-ABZ43216) and or GPCR proteins (ABP95596-ABS9594-BP95942) by extracting open-reading frames containing 6-8 transmembrane domains with 250-1000 amino acid residues to give a gene homologous with a known GPCR gene. The receptor proteins and encoded genes are useful for studying in vivo signal transduction mechanism and identifying targets for drug development e.g. based on olfactory and gustatory receptors in form of agonists and antagonists by screening intrins, and extrinsic ligands as bitter taste inhibitors, taste enhancers and fragarance 840 840 006 900 960 960 720 780 780 ATTITGACTGCAACTACTITCTGCCTCCCTTGGTGATAGTGACACTTTGCTATACCACG 660 R, G protein coupled receptor; signal transduction; olfactory; opment; gustatory; taste; fragrance; gene; ds. cardaadciracarcerricradaccarradcrecrercaacaccrrrregraaccrerra CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA AGGGTCATTCGGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATC CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTA AGGCTAACCATTCTGCTACTCGTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTG Database global search for G protekn-coupled receptors, proteins and encoded genes for studying in vivo signal transduction mechanism and identifying targets for drug development. GTAAGCGGGAACCTTGAGCAAGCAAAGAAATTAGTTACTCAAACAACCCTTGA 1014 961 GTAAGCGGGAACCTTGAGCAAAGAAAATTAGTTACTCAAACAACCCTTGA 1014 sting; Japanese. SEQ ID NO 13; 97pp + Sequence GPCR polynucleotide SEQ ID NO 13 (NISC-) JAPAN SCI & TECHNOLOGY CORP. 04-AUG-2000; 2000JP-00237818. 13-FEB-2001; 2001JP-00034434. IB001446. ABZ42876 standard; DNA; 1014 (first entry) WPI; 2002-304118/34. P-PSDB; ABP95602. 30-JUL-2001; 2001WO Takeda S, PCR; G WO200216548-A2 06-MAR-2003 28-FEB-2002. Homo sapien drug deve BZ42876; 901 Claim 9; 781 841 841 961 Haga T, 721 781 901 199 501 Human; Human RESULT ò 엄 g g ઠે g ò g ò ઠ